

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 16, 2003, 16:37:55 ; Search time 1447.31 Seconds
(without alignments)
15778.007 Million cell updates/sec

Title: US-09-497-967-102

Perfect score: 1410

Sequence: 1 atgaagaacaacatctcgtt.....cttactacctgctgtaataa 1410

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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EST: *
1: em_estba:*
2: em_estbthum:*
3: em_estinu:*
4: em_estinu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	57.2	4.1	502	B0134889	B0134889 INIT1_1_D
C 2	57.2	4.1	590	B0135179	B0135179 INIT1_4_C
C 3	57.2	4.1	602	B0135164	B0135164 INIT1_4_B
C 4	57.2	4.1	607	B0134912	B0134912 INIT1_1_F
C 5	56.8	4.0	658	B0135057	B0135057 INIT1_2_G
C 6	54	3.8	445	B0134871	B0134871 INIT1_1_B

C 7	52.4	3.7	419	14	B0135036	B0135036 INIT1_2_D
C 8	40	2.8	210	14	B0134900	B0134900 INIT1_1_E
C 9	40	2.8	538	14	B0134810	B0134810 INIT1_4_C
C 10	40	2.8	592	14	B0134985	B0134985 INIT1_2_G
C 11	40	2.8	599	14	B0134821	B0134821 INIT1_4_D
C 12	40	2.8	661	14	B0135189	B0135189 INIT1_4_D
C 13	40	2.8	675	14	B0135196	B0135196 INIT1_4_E
C 14	40	2.8	856	9	AL529709	AL529709 AL529709
C 15	39.8	2.8	565	12	BF191747	BF191747 239419 MA
C 16	39.4	2.8	946	17	CNS06063	AL10257 T7 end of
C 17	38.6	2.7	938	13	BI950738	BI950738 HVSME1002
C 18	37.8	2.7	390	13	BI316601	BI316601 HVS0509
C 19	37.8	2.7	997	17	CNS06066	AL11124 T7 end of
C 20	37.8	2.7	1089	17	CNS062J	AL10021 T3 end of
C 21	37.6	2.7	479	12	BF776376	BF776376 287167 MA
C 22	37.4	2.7	413	12	EG156079	EG156079 saa80a12
C 23	37.4	2.7	977	17	CNS02AMA	AL188731 Tetraodon
C 24	37.2	2.6	941	17	CNS056AV	AL322104 Tetraodon
C 25	37	2.6	1177	13	CG915930	CG915930 602815385
C 26	36.8	2.6	877	17	CNS04NWK	AL299261 Tetraodon
C 27	36.6	2.6	328	10	BB497602	BB497602 BB497602
C 28	36.4	2.6	576	9	AL818926	AL818926 AL818926
C 29	36.2	2.6	389	10	AW325085	AW325085 TENUA390
C 30	36.2	2.6	448	12	BF255972	BF255972 HVSMEF000
C 31	36.2	2.6	473	13	BM098087	BM098087 EBP103 SQ
C 32	36.2	2.6	576	12	CG301223	CG301223 HVSMEB001
C 33	36.2	2.6	688	9	A1612588	A1612588 TENG0393
C 34	36.2	2.6	791	9	AJ443260	AJ443260 AJ443260
C 35	36.2	2.6	894	12	CG367203	CG367203 HVSME1001
C 36	35.8	2.5	256	12	CG301587	CG301587 kt02H09.Y
C 37	35.8	2.5	273	13	BM339376	BM339376 MEST240-F
C 38	35.8	2.5	424	9	A1438101	A1438101 sa35h11.Y
C 39	35.8	2.5	447	12	BF707190	BF707190 282711 MA
C 40	35.8	2.5	513	10	BE355071	BE355071 BCL113-G
C 41	35.8	2.5	654	13	BI874624	BI874624 963116H11
C 42	35.8	2.5	669	9	AU169066	AU169066 AU169066
C 43	35.8	2.5	713	17	AZ346186	AZ346186 1M0081G06
C 44	35.8	2.5	862	12	BG769770	BG769770 602744673
C 45	35.8	2.5	920	12	BG420157	BG420157 602452258

ALIGNMENTS

RESULT 1
BQ134889/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BQ134889 502 bp mRNA linear EST 22-APR-2002
INIT1_1_D07.bl.A006.G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.
BQ134889
BQ134889.1 GI:20260988
EST.
Ichthyophthirius multifiliis.
Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
1 (bases 1 to 502)
Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,
Dickerson, H., Lin, T.-L. and Pratt, L.H.
An EST database for Ichthyophthirius multifiliis (G5 isolate)
Unpublished (2002)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 474

```

Seq primer: T7
High quality sequence start: 43
High quality sequence stop: 590
POLYA=No.

FEATURES
    source             Location/Qualifiers
        1..590
            /organism="Ichthyophthirius multifiliis"
            /strain="G5"
            /db_xref="taxon:5932"
            /clone_lib="G5 trophont cDNA (INIT1)"
            /note="Vector: pBluescript SK(-) from Lambda Zap II;
            Site_1: EcoRI; Site_2: EcoRI; The library was made from
            trophont polyA+ RNA of the G5 parasite strain.
            Double-stranded cDNA was linked to EcoRI adaptors, size
            fractionated, and material >500 bp cloned into lambda ZAP
            II. Plasmid DNA for sequencing was prepared by mass
            excision."

BASE COUNT      207 a    94 g    186 t
ORIGIN
Query Match      4.1%; Score 57.2; DB 14; Length 590;
Best Local Similarity 52.0%; Pred. No. 0.00013;
Matches 159; Conservative 0; Mismatches 138; Indels 9; Gaps 1;

QY 1114 GCTACCTCTACCTACCAAGCAGGCTGCTGAGTGTCTGGAACCGTCTGACCGACGGA 1173
Db 379 GCTACTTCAGCCACATAATGTTAAACGATTGCCCTGCTGTACAGTGGTTGATGATGGT 320
QY 1174 ACCACCTCTACCTACCAAGCAGGCTGCTGAGTGTCTGGAACCGTCTGACCGACGGA 1233
Db 319 ACATCAACTAATTTTGTAGCTTTAGCAAGTGAATGTAATGTTAGGCTAACTTTTAT 260
QY 1234 ACCACCAAGCAGACCGAGTGGTCTGGAATCGACACCTGTACCTCTGTAACAAGAG 1293
Db 259 GCATCAAAAACATCTGGTTTGCAGCAGGTACTGATACATGATGATGTTCTTAAAAA 200
QY 1294 CTGACCTCTGGAGTGGAGTAACTGCTGAGTGTCTGTAAGAAGACATCCAGTGTAC 1353
Db 199 TTAACCTCTGGTGTACAGCTAAAGTATATGCTGAAGCTACTTAAAGACATAATGCGCC 140
QY 1354 -----TTGCGTAACTTCCTGCTCTATCTCTGCTGCTGATCTCTTACTACCTGCTG 1404
Db 139 AGTTCCACTTTTCGAAAAATTTTATCAATGCTCCTTAATATTTATTTCTTTCTTTG 80
QY 1405 TAATAA 1410
Db 79 TGATGA 74

RESULT 2
BQ135179/c
LOCUS      BQ135179      590 bp      mRNA      linear      EST 22-APR-2002
DEFINITION      INIT1.4.C08.g1.A006.G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.
ACCESSION      BQ135179.1      GI:20261278
VERSION      BQ135179
KEYWORDS
SOURCE      EST.
ORGANISM      Ichthyophthirius multifiliis.
            Ichthyophthirius multifiliis
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Ophryoglenina; Ichthyophthirius.
            1 (bases 1 to 590)
            Clark.T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
            Dickerson,H., Lin,T.-L. and Pratt,L.H.
            An EST database for Ichthyophthirius multifiliis (G5 isolate)
            Unpublished (2002)
            Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            Sequences have been trimmed to exclude polyA, vector, and regions
            below Phred quality 16. The threshold for highest quality sequence
            is 20.

FEATURES
    source             Location/Qualifiers
        1..502
            /organism="Ichthyophthirius multifiliis"
            /strain="G5"
            /db_xref="taxon:5932"
            /clone_lib="G5 trophont cDNA (INIT1)"
            /note="Vector: pBluescript SK(-) from Lambda Zap II;
            Site_1: EcoRI; Site_2: EcoRI; The library was made from
            trophont polyA+ RNA of the G5 parasite strain.
            Double-stranded cDNA was linked to EcoRI adaptors, size
            fractionated, and material >500 bp cloned into lambda ZAP
            II. Plasmid DNA for sequencing was prepared by mass
            excision."

BASE COUNT      185 a    80 c    70 g    167 t
ORIGIN
Query Match      4.1%; Score 57.2; DB 14; Length 502;
Best Local Similarity 52.0%; Pred. No. 0.00012;
Matches 159; Conservative 0; Mismatches 138; Indels 9; Gaps 1;

QY 1114 GCTACCTGATCCTCAGTGTCTGAGTGTCTGGAACCGTCTGACCGACGGA 1173
Db 379 GCTACTTCAGCCACATAATGTTAAACGATTGCCCTGCTGTACAGTGGTTGATGATGGT 320
QY 1174 ACCACCTCTACCTACCAAGCAGGCTGCTGAGTGTCTGGAACCGTCTGACCGACGGA 1233
Db 319 ACATCAACTAATTTTGTAGCTTTAGCAAGTGAATGTAATGTTAGGCTAACTTTTAT 260
QY 1234 ACCACCAAGCAGACCGAGTGGTCTGGAATCGACACCTGTACCTCTGTAACAAGAG 1293
Db 259 GCATCAAAAACATCTGGTTTGCAGCAGGTACTGATACATGATGATGTTCTTAAAAA 200
QY 1294 CTGACCTCTGGAGTGGAGTAACTGCTGAGTGTCTGTAAGAAGACATCCAGTGTAC 1353
Db 199 TTAACCTCTGGTGTACAGCTAAAGTATATGCTGAAGCTACTTAAAGACATAATGCGCC 140
QY 1354 -----TTGCGTAACTTCCTGCTCTATCTCTGCTGCTGATCTCTTACTACCTGCTG 1404
Db 139 AGTTCCACTTTTCGAAAAATTTTATCAATGCTCCTTAATATTTATTTCTTTCTTTG 80
QY 1405 TAATAA 1410
Db 79 TGATGA 74

RESULT 3
BQ135164/c
LOCUS      BQ135164      602 bp      mRNA      linear      EST 22-APR-2002
DEFINITION      INIT1.4.B05.g1.A006.G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.
ACCESSION      BQ135164
VERSION      BQ135164.1      GI:20261263
KEYWORDS      EST.
SOURCE      Ichthyophthirius multifiliis.
            Ichthyophthirius multifiliis
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Ophryoglenina; Ichthyophthirius.
            1 (bases 1 to 602)
            Clark.T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
            Dickerson,H., Lin,T.-L. and Pratt,L.H.
            An EST database for Ichthyophthirius multifiliis (G5 isolate)
            Unpublished (2002)
            Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            Sequences have been trimmed to exclude polyA, vector, and regions
            below Phred quality 16. The threshold for highest quality sequence
            is 20.

```


Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20.

Seq primer: JEN REV

High quality sequence stop: 531

POLYA=No.

FEATURES

source

Location/Qualifiers

1..538
/organism="Ichthyophthirius multifiliis"
/strain="G5"

/db_xref="taxon:5932"

/clone_lib="G5 trophont cDNA (INIT1)"

/note="Vector: pBluescript SK(-) from Lambda Zap II;

Site_1: EcoRI; Site_2: EcoRI; The library was made from

trophont polyA+ RNA of the G5 parasite strain.

Double-stranded cDNA was linked to EcoRI adaptors, size

fractionated, and material >500 bp cloned into lambda ZAP

II. Plasmid DNA for sequencing was prepared by mass

excision."

155 a 101 c 106 g 175 t 1 others

BASE COUNT
ORIGIN

Query Match 2.8%; Score 40; DB 14; Length 538;

Best Local Similarity 58.3%; Pred. No. 6.1;

Matches 70; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1114 GCTACCCCTGATCGTCAGTGTCTCTGGAGTGTCTGCTGGAACGCTGCTGACCGACGGA 1173

Db 231 GCTAATTAGCCGCAATATGTGGCACTGAATGCTCTGCTGGCACTCTGTTTACAGACGGA 290

QY 1174 ACCACCTTACCTACACGAGCGCTCTCTGAGTGTGTGAAGTGTGCTTAACCTCTAC 1233

Db 291 GTAACACCTACTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 350

RESULT 10
BQ134985

LOCUS INIT1_2.G01.bl_A006 G5 trophont cDNA (INIT1) Ichthyophthirius

DEFINITION multifiliis cDNA, mRNA sequence. EST 22-APR-2002

ACCESSION BQ134985

VERSION BQ134985.1 GI:20261084

KEYWORDS EST.

SOURCE Ichthyophthirius multifiliis.

ORGANISM

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;

Hymenostomatida; Ophryoglenina; Ichthyophthirius.

1 (bases 1 to 592)

Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,

Dickerson, H., Lin, T.-L. and Pratt, L.H.

An EST database for Ichthyophthirius multifiliis (G5 isolate)

Unpublished (2002)

TITLE

JOURNAL

COMMENT

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector, and regions

below Phred quality 16. The threshold for highest quality sequence

is 20.

Seq primer: JEN REV

High quality sequence stop: 575

POLYA=No.

Location/Qualifiers

1..592

/organism="Ichthyophthirius multifiliis"

/strain="G5"

/db_xref="taxon:5932"

/clone_lib="G5 trophont cDNA (INIT1)"

/note="Vector: pBluescript SK(-) from Lambda Zap II;

Site_1: EcoRI; Site_2: EcoRI; The library was made from

trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda ZAP
II. Plasmid DNA for sequencing was prepared by mass
excision."

BASE COUNT 179 a 114 c 110 g 189 t

ORIGIN

Query Match 2.8%; Score 40; DB 14; Length 592;

Best Local Similarity 58.3%; Pred. No. 6.4;

Matches 70; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1114 GCTACCCCTGATCGTCAGTGTCTCTGGAGTGTCTGCTGGAACGCTGCTGACCGACGGA 1173

Db 371 GCTAATTAGCCGCAATATGTGGCACTGAATGCTCTGCTGGCACTCTGTTTACAGACGGA 430

QY 1174 ACCACCTTACCTACACGAGCGCTCTCTGAGTGTGTGAAGTGTGCTGCTTAACCTCTAC 1233

Db 431 GTAACACCTACTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 490

RESULT 11

BQ134821/c

LOCUS

DEFINITION

multifiliis cDNA, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector, and regions

below Phred quality 16. The threshold for highest quality sequence

is 20.

Seq primer: JEN REV

High quality sequence stop: 506

POLYA=No.

Location/Qualifiers

1..599

/organism="Ichthyophthirius multifiliis"

/strain="G5"

/db_xref="taxon:5932"

/clone_lib="G5 trophont cDNA (INIT1)"

/note="Vector: pBluescript SK(-) from Lambda Zap II;

Site_1: EcoRI; Site_2: EcoRI; The library was made from

trophont polyA+ RNA of the G5 parasite strain.

Double-stranded cDNA was linked to EcoRI adaptors, size

fractionated, and material >500 bp cloned into lambda ZAP

II. Plasmid DNA for sequencing was prepared by mass

excision."

191 a 113 c 111 g 183 t 1 others

BASE COUNT

ORIGIN

Query Match 2.8%; Score 40; DB 14; Length 599;

Best Local Similarity 58.3%; Pred. No. 6.4;

Matches 70; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1114 GCTACCCCTGATCGTCAGTGTCTCTGGAGTGTCTGCTGGAACGCTGCTGACCGACGGA 1173

Db 1114 GCTACCCCTGATCGTCAGTGTCTCTGGAGTGTCTGCTGGAACGCTGCTGACCGACGGA 1173


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1. .565
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2Pig"
/tissue_type="pooled"
/lab_host="DH10B"
/notes="vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT 115 a 147 c 141 t 1 others
ORIGIN
Query Match 2.8%; Score 39.8; DB 12; Length 565;
Best Local Similarity 50.0%; Pred. No. 7.1;
Matches 98; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
QY 1022 TGCAGCGAACAACCTCCAGCGTGGATCTTCTCGCTGTAAAGCTGTGCTCGCTAACAAAGG 1081
DB 313 TCTAGGAAGAAATCCCTCGAAGGAAGTACCATTGAGGGCTCTGCATAAAACATGA 372
QY 1082 TGCAGGGAGCTGTGGCTACCGCTGGAGAACGGCTACCGCTGATCGCTCAGTGTGCTCTGG 1141
DB 373 ATACGGGGGGGGGGGATGTGGAGGAGGGGCTCGCGGGGGACCCCTGTGTCTGT 432
QY 1142 AGTGTCTCTGGACCGTGTGACCGAGGAAACCACTCTACCTACAAGCAGGCTGCTT 1201
DB 433 TTGTGTCTTGTGAGCGTTTGCCAGGCAGATACCCCTTCACCTTCCTGTACCCGGAGT 492
QY 1202 CTGAGTGTGTGAAGTG 1217
DB 493 TTCCTGGACGAGCTG 508
Search completed: February 16, 2003, 22:25:24
Job time : 1457.31 secs

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RESULT 15	BF191747	565 bp	linear	EST 02-NOV-2000
LOCUS	239419	MARC 2P1G	Sus scrofa cDNA 5', mRNA sequence.	
DEFINITION	BF191747			
ACCESSION	BF191747.1	GI:11075116		
VERSION	EST.			
KEYWORDS	pig.			
SOURCE	Sus scrofa			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
REFERENCE	1 (bases 1 to 565)			
AUTHORS	Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.			
TITLE	Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov			
FEATURES	Single pass sequencing. Bases called and alt.trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options. PCR Primers FORWARD: AGGAACACAGCTATGACCAT BACKWARD: GTTTCGCAGTCACGCG Plate: 67 row: 0 column: 16 Seq primer: ATTTAGGTGACACTATAG. Location/Qualifiers			